1806

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/612,929

CRF Processing Date: 3/6/97
Edited by: _____
Verified by: _____ (STIC staff)

ENTERED #9 Dennis 3/11/97

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☑ Edited the Current Application Data section with the actual current number. The ~~number~~ numbers inputted by the applicant was/were ☒ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

This Raw Listing contains the General Information Section and up to the first 5 pages.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.

(ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: Corporate Intellectual Property, UW2220 - 709 Swedeland Rd.
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
--> **(A) APPLICATION NUMBER: US 08/117,366**
(B) FILING DATE: 07-SEP-1994
(C) CLASSIFICATION:

--> **(A) APPLICATION NUMBER: US 08/136,783**
(B) FILING DATE: 14-OCT-1993
(C) CLASSIFICATION:

(vii) PRIOR:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Sutton, Jeffrey A.
(B) REGISTRATION NUMBER: 34,028
(C) REFERENCE/DOCKET NUMBER: P50186-2

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (215) 270-5024
(B) TELEFAX: (215) 270-5090

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA        48
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1               5                  10                  15

GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT        96
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
            20                  25                  30

GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT       144
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
        35                  40                  45

GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA       192
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
    50                  55                  60

GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT       240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
65                  70                  75                  80

GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC       288
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95

CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT       336
Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
            100                 105                 110

CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG       384
Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
```

```
100          115                 120                 125
101
102   GAA ATC AAA CGG                                                396
103   Glu Ile Lys Arg
104       130
105
106
107   (2) INFORMATION FOR SEQ ID NO:2:
108
109         (i) SEQUENCE CHARACTERISTICS:
110               (A) LENGTH: 132 amino acids
111               (B) TYPE: amino acid
112               (D) TOPOLOGY: linear
113
114        (ii) MOLECULE TYPE: protein
115
116        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
117
118   Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
119     1               5                  10                  15
120
121   Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
122                20                  25                  30
123
124   Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
125            35                  40                  45
126
127   Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
128        50                  55                  60
129
130
131   Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
132    65                  70                  75                  80
133
134   Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
135                    85                  90                  95
136
137   Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
138                100                 105                 110
139
140   Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
141            115                 120                 125
142
143   Glu Ile Lys Arg
144       130
145
146
147   (2) INFORMATION FOR SEQ ID NO:3:
148
149        (i) SEQUENCE CHARACTERISTICS:
150             (A) LENGTH: 483 base pairs
151             (B) TYPE: nucleic acid
152             (C) STRANDEDNESS: double
```

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 64..483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GAATTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA      60

GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA      108
    Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala
      1               5                  10                  15

TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG      156
Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
                  20                  25                  30

CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA      204
Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
              35                  40                  45

CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA      252
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
          50                  55                  60

AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC      300
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
      65                  70                  75

TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC      348
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
  80                  85                  90                  95

AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT      396
Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
                 100                 105                 110

GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC      444
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
             115                 120                 125

GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA                  483
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
         130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala Tyr
 1               5                  10                  15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
            20                  25                  30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
        35                  40                  45

Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
    50                  55                  60

Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
65                  70                  75                  80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
                85                  90                  95

Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
            100                 105                 110

Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
        115                 120                 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/612,929*

INPUT SET: S15989.raw

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: US 08/117,366
34	Wrong application Serial Number	(A) APPLICATION NUMBER: US 08/136,783